

SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 HUMAN SERVICES, CENTERS FOR DISEASE CONTROL AND PREVENTION
 Lal, Renu B.
 Owen, Sherry M.

<120> IMMUNOGENIC HIV-1 MULTI-CLADE, MULTIVALENT CONSTRUCTS AND METHODS
 OF THEIR USE

<130> 6395-67675

<150> US 60/458,880

<151> 2003-03-28

<160> 64

<170> PatentIn version 3.2

<210> 1

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> Construct encoding polyepitope polypeptide.

<220>

<221> CDS

<222> (12)..(1547)

<223> Sequence encoding MCMVCTL-ubiquitin polyepitope polypeptide.

<400> 1

ctaggctagc t atg cag atc ttc gtg aaa acc ctt acc ggc aag acc atc	50
Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile	
1 5 10	
acc ctt gag gtg gag ccc agt gac acc atc gaa aat gtg aag gcc aag	98
Thr Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys	
15 20 25	
atc cag gat aag gaa ggc att ccc ccc gac cag cag agg ctc atc ttt	146
Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe	
30 35 40 45	
gca ggc aag cag ctg gaa gat ggc cgt act ctt tct gac tac aac atc	194
Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile	
50 55 60	
cag aag gag tcg acc ctg cac ctg gtc ctg cgt ctg aga ggt gct gag	242
Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Glu	
65 70 75	
ctc cgc tcc ctc tac aac acc gtg gcc acc ctc tac tgc gtg cac cag	290
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln	
80 85 90	
cgc atc aag atc cgc ctg cgc ccc ggc ggc aag aag aag tac tgg gcc	338
Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Trp Ala	

95	100	105	
agc cgc gag ctg gag cgc ttc aag gcc gcc atc agc ccc cgc acc ctg Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg Thr Leu 110 115 120 125			386
aac gcc tgg gtg aag gtg gtg aag gcc ttc agc ccc gag gtg atc ccc Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro Glu Val Ile Pro 130 135 140			434
atg ttc agc gcc ctg agc gag ggc gcc acc ccc cag gac ctg aac acc Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr 145 150 155			482
atg acc agc acc ctg cag gag cag atc ggc tgg aag gcc gcc aac ccc Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala Asn Pro 160 165 170			530
ccc atc ccc gtg ggc gac atc tac aag cgc tgg atc atc ctg ggc ctg Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu 175 180 185			578
aac aag atc gtg cgc atg tac agc ccc acc agc atc ttc cgc gac tac Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg Asp Tyr 190 195 200 205			626
gtg gac cgc ttc tac aag acc ctg cgc gcc gtg cag aac gcc aac ccc Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala Asn Pro 210 215 220			674
gac tgc aag acc atc ctg aag gcc ctg gcc tgc cag ggc gtg ggc ggc Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val Gly Gly 225 230 235			722
ccc ggc cac aag aag gcc gcc atc acc ctg tgg cag cgc ccc ctg gtg Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro Leu Val 240 245 250			770
acc gtg ctg gac gtg ggc gac gcc tac ttc agc gtg tgg aag ggc agc Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys Gly Ser 255 260 265			818
ccc gcc atc ttc cag agc aag ctt cgc ggc ccc ggc cgc gcc ttc gtg Pro Ala Ile Phe Gln Ser Lys Leu Arg Gly Pro Gly Arg Ala Phe Val 270 275 280 285			866
acc atc aag gcc gcc gcc tgc acc ccc tac gac atc aac cag atg ctg Thr Ile Lys Ala Ala Ala Cys Thr Pro Tyr Asp Ile Asn Gln Met Leu 290 295 300			914
ggt acc agc atg acc aag atc ctg aag gag ccc gtg cac ggc gtg aag Gly Thr Ser Met Thr Lys Ile Leu Lys Glu Pro Val His Gly Val Lys 305 310 315			962
gcc gcc cag atc tac cag gag ccc ttc aag aac ctg aag acc ggc gag Ala Ala Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Glu 320 325 330			1010
ccc atc gtg ggc gcc gag acc ttc tac gtg gac ggc gcc gcc aac gtg Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Val 335 340 345			1058

atc tac cag tac atg gac gac ctg ctg ctg tgg aag ggc gag ggc gcc 1106
 Ile Tyr Gln Tyr Met Asp Asp Leu Leu Leu Trp Lys Gly Glu Gly Ala
 350 355 360 365

gtg aag gcc gcc cgc atc cgc acc tgg aag agc ctg gtg aag cac ccc 1154
 Val Lys Ala Ala Arg Ile Arg Thr Trp Lys Ser Leu Val Lys His Pro
 370 375 380

aag gtg agc agc gag gtg cac atc gcc gtg cgc cac ttc ccc cgc atc 1202
 Lys Val Ser Ser Glu Val His Ile Ala Val Arg His Phe Pro Arg Ile
 385 390 395

tgg gcc gtg cgc cac ttc ccc cgc ccc tgg gcc atc atc cgc atc ctg 1250
 Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala Ile Ile Arg Ile Leu
 400 405 410

cag cag ctg aag gcc gcc gtg ggc ttc ccc gtg cgc ccc cag gtg ccc 1298
 Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val Arg Pro Gln Val Pro
 415 420 425

ctg cgc ccc atg acc tac aag ggc gcc gtg gac ctg agc cac ttc ctg 1346
 Leu Arg Pro Met Thr Lys Gly Ala Val Asp Leu Ser His Phe Leu
 430 435 440 445

aag gag aag ggc ggc ctg ggc ccc ggc gtg cgc tac ccc ctg acc ttc 1394
 Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe
 450 455 460

ggc tgg tgc tac aag gcc gcc aag acc ctg ccc ctg tgc gtg acc ctg 1442
 Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro Leu Cys Val Thr Leu
 465 470 475

acc gtg tac tac ggc gtg ccc gtg tgg aag gag gcc acc acc acc ctg 1490
 Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
 480 485 490

cgc gcc atc gag gcc cag cag cac ctg gag cgc tac ctg aag gac ggc 1538
 Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg Tyr Leu Lys Asp Gly
 495 500 505

ggc ctg tag ctgagtagc 1557
 Gly Leu
 510

<210> 2
 <211> 511
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Construct encoding polypeptide.

<400> 2

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
 1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp

20	25	30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys		
35	40	45
Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu		
50	55	60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Glu Leu Arg Ser		
65	70	75
Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Lys		
85	90	95
Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Trp Ala Ser Arg Glu		
100	105	110
Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp		
115	120	125
Val Lys Val Val Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser		
130	135	140
Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Thr Ser		
145	150	155
Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala Asn Pro Pro Ile Pro		
165	170	175
Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile		
180	185	190
Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg Asp Tyr Val Asp Arg		
195	200	205
Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala Asn Pro Asp Cys Lys		
210	215	220
Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val Gly Gly Pro Gly His		
225	230	235
Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Leu		
245	250	255
Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys Gly Ser Pro Ala Ile		
260	265	270

Phe Gln Ser Lys Leu Arg Gly Pro Gly Arg Ala Phe Val Thr Ile Lys
 275 280 285

Ala Ala Ala Cys Thr Pro Tyr Asp Ile Asn Gln Met Leu Gly Thr Ser
 290 295 300

Met Thr Lys Ile Leu Lys Glu Pro Val His Gly Val Lys Ala Ala Gln
 305 310 315 320

Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Glu Pro Ile Val
 325 330 335

Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Val Ile Tyr Gln
 340 345 350

Tyr Met Asp Asp Leu Leu Leu Trp Lys Gly Glu Gly Ala Val Lys Ala
 355 360 365

Ala Arg Ile Arg Thr Trp Lys Ser Leu Val Lys His Pro Lys Val Ser
 370 375 380

Ser Glu Val His Ile Ala Val Arg His Phe Pro Arg Ile Trp Ala Val
 385 390 395 400

Arg His Phe Pro Arg Pro Trp Ala Ile Ile Arg Ile Leu Gln Gln Leu
 405 410 415

Lys Ala Ala Val Gly Phe Pro Val Arg Pro Gln Val Pro Leu Arg Pro
 420 425 430

Met Thr Tyr Lys Gly Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
 435 440 445

Gly Gly Leu Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
 450 455 460

Tyr Lys Ala Ala Lys Thr Leu Pro Leu Cys Val Thr Leu Thr Val Tyr
 465 470 475 480

Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Arg Ala Ile
 485 490 495

Glu Ala Gln Gln His Leu Glu Arg Tyr Leu Lys Asp Gly Gly Leu
 500 505 510

<210> 3
 <211> 1323
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Construct encoding polyepitope polypeptide.

 <220>
 <221> CDS
 <222> (7)..(1317)
 <223> Sequence encoding MCMVCTL (no ubiquitin) polyepitope polypeptide.

 <400> 3
 gctagc atg gag ctc cgc tcc ctc tac aac acc gtg gcc acc ctc tac 48
 Met Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr
 1 5 10

 tgc gtg cac cag cgc atc aag atc cgc ctg cgc ccc gcc gcc aag aag 96
 Cys Val His Gln Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys
 15 20 25 30

 aag tac tgg gcc agc cgc gag ctg gag cgc ttc aag gcc gcc atc agc 144
 Lys Tyr Trp Ala Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser
 35 40 45

 ccc cgc acc ctg aac gcc tgg gtg aag gtg gtg aag gcc ttc agc ccc 192
 Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro
 50 55 60

 gag gtg atc ccc atg ttc agc gcc ctg agc gag gcc gcc acc ccc cag 240
 Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
 65 70 75

 gac ctg aac acc atg acc agc acc ctg cag gag cag atc gcc tgg aag 288
 Asp Leu Asn Thr Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys
 80 85 90

 gcc gcc aac ccc ccc atc ccc gtg gcc gac atc tac aag cgc tgg atc 336
 Ala Ala Asn Pro Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile
 95 100 105 110

 atc ctg gcc ctg aac aag atc gtg cgc atg tac agc ccc acc agc atc 384
 Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
 115 120 125

 ttc cgc gac tac gtg gac cgc ttc tac aag acc ctg cgc gcc gtg cag 432
 Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln
 130 135 140

 aac gcc aac ccc gac tgc aag acc atc ctg aag gcc ctg gcc tgc cag 480
 Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln
 145 150 155

 gcc gtg gcc gcc ccc gcc cac aag aag gcc gcc atc acc ctg tgg cag 528
 Gly Val Gly Gly Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln
 160 165 170

 cgc ccc ctg gtg acc gtg ctg gac gtg gcc gac gcc tac ttc agc gtg 576

Arg	Pro	Leu	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val			
175					180					185					190			
tgg	aag	ggc	agc	ccc	gcc	atc	ttc	cag	agc	aag	ctt	cgc	ggc	ccc	ggc			624
Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Ser	Lys	Leu	Arg	Gly	Pro	Gly			
				195					200					205				
cgc	gcc	ttc	gtg	acc	atc	aag	gcc	gcc	gcc	tgc	acc	ccc	tac	gac	atc			672
Arg	Ala	Phe	Val	Thr	Ile	Lys	Ala	Ala	Ala	Cys	Thr	Pro	Tyr	Asp	Ile			
			210					215					220					
aac	cag	atg	ctg	ggt	acc	agc	atg	acc	aag	atc	ctg	aag	gag	ccc	gtg			720
Asn	Gln	Met	Leu	Gly	Thr	Ser	Met	Thr	Lys	Ile	Leu	Lys	Glu	Pro	Val			
		225					230						235					
cac	ggc	gtg	aag	gcc	gcc	cag	atc	tac	cag	gag	ccc	ttc	aag	aac	ctg			768
His	Gly	Val	Lys	Ala	Ala	Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu			
		240				245					250							
aag	acc	ggc	gag	ccc	atc	gtg	ggc	gcc	gag	acc	ttc	tac	gtg	gac	ggc			816
Lys	Thr	Gly	Glu	Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly			
		255			260					265				270				
gcc	gcc	aac	gtg	atc	tac	cag	tac	atg	gac	gac	ctg	ctg	ctg	tgg	aag			864
Ala	Ala	Asn	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Leu	Leu	Trp	Lys			
			275						280					285				
ggc	gag	ggc	gcc	gtg	aag	gcc	gcc	cgc	atc	cgc	acc	tgg	aag	agc	ctg			912
Gly	Glu	Gly	Ala	Val	Lys	Ala	Ala	Arg	Ile	Arg	Thr	Trp	Lys	Ser	Leu			
			290					295					300					
gtg	aag	cac	ccc	aag	gtg	agc	agc	gag	gtg	cac	atc	gcc	gtg	cgc	cac			960
Val	Lys	His	Pro	Lys	Val	Ser	Ser	Glu	Val	His	Ile	Ala	Val	Arg	His			
		305					310					315						
ttc	ccc	cgc	atc	tgg	gcc	gtg	cgc	cac	ttc	ccc	cgc	ccc	tgg	gcc	atc			1008
Phe	Pro	Arg	Ile	Trp	Ala	Val	Arg	His	Phe	Pro	Arg	Pro	Trp	Ala	Ile			
		320				325					330							
atc	cgc	atc	ctg	cag	cag	ctg	aag	gcc	gcc	gtg	ggc	ttc	ccc	gtg	cgc			1056
Ile	Arg	Ile	Leu	Gln	Gln	Leu	Lys	Ala	Ala	Val	Gly	Phe	Pro	Val	Arg			
					340					345				350				
ccc	cag	gtg	ccc	ctg	cgc	ccc	atg	acc	tac	aag	ggc	gcc	gtg	gac	ctg			1104
Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Gly	Ala	Val	Asp	Leu			
				355					360					365				
agc	cac	ttc	ctg	aag	gag	aag	ggc	ggc	ctg	ggc	ccc	ggc	gtg	cgc	tac			1152
Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Gly	Pro	Gly	Val	Arg	Tyr			
			370				375						380					
ccc	ctg	acc	ttc	ggc	tgg	tgc	tac	aag	gcc	gcc	aag	acc	ctg	ccc	ctg			1200
Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Ala	Ala	Lys	Thr	Leu	Pro	Leu			
			385				390						395					
tgc	gtg	acc	ctg	acc	gtg	tac	tac	ggc	gtg	ccc	gtg	tgg	aag	gag	gcc			1248
Cys	Val	Thr	Leu	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Ala			
		400				405					410							
acc	acc	acc	ctg	cgc	gcc	atc	gag	gcc	cag	cag	cac	ctg	gag	cgc	tac			1296
Thr	Thr	Thr	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Leu	Glu	Arg	Tyr			

415		420		425		430	
ctg aag gac ggc ggc	ctg tag ctcgag						1323
Leu Lys Asp Gly Gly	Leu						
	435						

```
<210> 4
<211> 436
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Construct encoding polypeptide polypeptide.

<400> 4

Met Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val
1 5 10 15

His Gln Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr
20 25 30

Trp Ala Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg
35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro Glu Val
50 55 60

Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu
65 70 75 80

Asn Thr Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala
85 90 95

Asn Pro Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu
100 105 110

Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg
115 120 125

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala
130 135 140

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val
145 150 155 160

Gly Gly Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro
165 170 175

Leu Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys
 180 185 190

Gly Ser Pro Ala Ile Phe Gln Ser Lys Leu Arg Gly Pro Gly Arg Ala
 195 200 205

Phe Val Thr Ile Lys Ala Ala Ala Cys Thr Pro Tyr Asp Ile Asn Gln
 210 215 220

Met Leu Gly Thr Ser Met Thr Lys Ile Leu Lys Glu Pro Val His Gly
 225 230 235 240

Val Lys Ala Ala Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
 245 250 255

Gly Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
 260 265 270

Asn Val Ile Tyr Gln Tyr Met Asp Asp Leu Leu Leu Trp Lys Gly Glu
 275 280 285

Gly Ala Val Lys Ala Ala Arg Ile Arg Thr Trp Lys Ser Leu Val Lys
 290 295 300

His Pro Lys Val Ser Ser Glu Val His Ile Ala Val Arg His Phe Pro
 305 310 315 320

Arg Ile Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala Ile Ile Arg
 325 330 335

Ile Leu Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val Arg Pro Gln
 340 345 350

Val Pro Leu Arg Pro Met Thr Tyr Lys Gly Ala Val Asp Leu Ser His
 355 360 365

Phe Leu Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg Tyr Pro Leu
 370 375 380

Thr Phe Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro Leu Cys Val
 385 390 395 400

Thr Leu Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr
 405 410 415

Thr Leu Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg Tyr Leu Lys

420

425

430

Asp Gly Gly Leu
435

<210> 5

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Polyepitope polypeptide.

<400> 5

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15

Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45

Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln Lys Glu
50 55 60

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Ala Glu Leu Arg Ser
65 70 75 80

Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Lys
85 90 95

Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Trp Ala Ser Arg Glu
100 105 110

Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp
115 120 125

Val Lys Val Val Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser
130 135 140

Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Thr Ser
145 150 155 160

Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala Asn Pro Pro Ile Pro
165 170 175

Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
 180 185 190

Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg Asp Tyr Val Asp Arg
 195 200 205

Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala Asn Pro Asp Cys Lys
 210 215 220

Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val Gly Gly Pro Gly His
 225 230 235 240

Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Leu
 245 250 255

Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys Gly Ser Pro Ala Ile
 260 265 270

Phe Gln Ser Lys Leu Gly Thr Ser Met Thr Lys Ile Leu Lys Glu Pro
 275 280 285

Val His Gly Val Lys Ala Ala Gln Ile Tyr Gln Glu Pro Phe Lys Asn
 290 295 300

Leu Lys Thr Gly Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp
 305 310 315 320

Gly Ala Ala Asn Val Ile Tyr Gln Tyr Met Asp Asp Leu Leu Leu Trp
 325 330 335

Lys Gly Glu Gly Ala Val Lys Ala Ala Arg Ile Arg Thr Trp Lys Ser
 340 345 350

Leu Val Lys His Pro Lys Val Ser Ser Glu Val His Ile Ala Val Arg
 355 360 365

His Phe Pro Arg Ile Trp Ala Val Arg His Phe Pro Arg Pro Trp Ala
 370 375 380

Ile Ile Arg Ile Leu Gln Gln Leu Lys Ala Ala Val Gly Phe Pro Val
 385 390 395 400

Arg Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Gly Ala Val Asp
 405 410 415

Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Gly Pro Gly Val Arg

420 425 430
 Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Ala Ala Lys Thr Leu Pro
 435 440 445
 Leu Cys Val Thr Leu Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu
 450 455 460
 Ala Thr Thr Thr Leu Arg Ala Ile Glu Ala Gln Gln His Leu Glu Arg
 465 470 475 480
 Tyr Leu Lys Asp Gly Gly Leu
 485

<210> 6
 <211> 412
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Polyepitope polypeptide.
 <400> 6

Met Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val
 1 5 10 15

His Gln Arg Ile Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr
 20 25 30

Trp Ala Ser Arg Glu Leu Glu Arg Phe Lys Ala Ala Ile Ser Pro Arg
 35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Lys Ala Phe Ser Pro Glu Val
 50 55 60

Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu
 65 70 75 80

Asn Thr Met Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Lys Ala Ala
 85 90 95

Asn Pro Pro Ile Pro Val Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu
 100 105 110

Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Phe Arg
 115 120 125

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Val Gln Asn Ala
 130 135 140

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Ala Cys Gln Gly Val
 145 150 155 160

Gly Gly Pro Gly His Lys Lys Ala Ala Ile Thr Leu Trp Gln Arg Pro
 165 170 175

Leu Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Trp Lys
 180 185 190

Gly Ser Pro Ala Ile Phe Gln Ser Lys Leu Gly Thr Ser Met Thr Lys
 195 200 205

Ile Leu Lys Glu Pro Val His Gly Val Lys Ala Ala Gln Ile Tyr Gln
 210 215 220

Glu Pro Phe Lys Asn Leu Lys Thr Gly Glu Pro Ile Val Gly Ala Glu
 225 230 235 240

Thr Phe Tyr Val Asp Gly Ala Ala Asn Val Ile Tyr Gln Tyr Met Asp
 245 250 255

Asp Leu Leu Leu Trp Lys Gly Glu Gly Ala Val Lys Ala Ala Arg Ile
 260 265 270

Arg Thr Trp Lys Ser Leu Val Lys His Pro Lys Val Ser Ser Glu Val
 275 280 285

His Ile Ala Val Arg His Phe Pro Arg Ile Trp Ala Val Arg His Phe
 290 295 300

Pro Arg Pro Trp Ala Ile Ile Arg Ile Leu Gln Gln Leu Lys Ala Ala
 305 310 315 320

Val Gly Phe Pro Val Arg Pro Gln Val Pro Leu Arg Pro Met Thr Tyr
 325 330 335

Lys Gly Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu
 340 345 350

Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Ala
 355 360 365

Ala Lys Thr Leu Pro Leu Cys Val Thr Leu Thr Val Tyr Tyr Gly Val

370

375

380

Pro Val Trp Lys Glu Ala Thr Thr Thr Leu Arg Ala Ile Glu Ala Gln
 385 390 395 400

Gln His Leu Glu Arg Tyr Leu Lys Asp Gly Gly Leu
 405 410

<210> 7

<211> 2126

<212> DNA

<213> Artificial Sequence

<220>

<223> Construct encoding polyepitope polypeptide.

<220>

<221> CDS

<222> (7)..(2118)

<223> Sequence encoding MCMVABTh-LIMPPII polyepitope polypeptide.

<400> 7

gctagc atg gcc tgc acc aac tgc tac tgc aag aag tgc tgc ttc cac 48
 Met Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
 1 5 10

tgc cag gtg tgc ttc acc acc ggc ccc ggc ccc cgc cag cgc cgc cgc 96
 Cys Gln Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg
 15 20 25 30

gcc ccc cag gac agc cag acc cac cag gtg agc gta tac tac gcc gcc 144
 Ala Pro Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala
 35 40 45

gcc cag tgg gac ttc ggc aac acc atg tgc cag atc aat ccc ggc cgc 192
 Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg
 50 55 60

agc cag aag gag ggc ctg cac tac acc tgc gta tac ggc ccc ggc ccc 240
 Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro
 65 70 75

ccc tgc aac aag tgc tac tgc aag aag tgc tgc tac cac tgc cag gtg 288
 Pro Cys Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val
 80 85 90

tgc ttc ctg aac aat ccc ggc aag cag cgc cgc ggc acc ccc cag agc 336
 Cys Phe Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser
 95 100 105 110

aac aag gac cac cag aac ccc ggc cct gga ccc aac gag cag gac ctg 384
 Asn Lys Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu
 115 120 125

ctg gcc ctg gac aag tgg gcc aac ctg tgg aac tgg ttc gac atc agc 432
 Leu Ala Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser
 130 135 140

aat ccc ggc gcc tgc aac acc tgc tac tgc aag aag tgc agc tac cac Asn Pro Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His 145 150 155	480
tgc ctg gtg tgc ttc cag acc ggc ccc ggc ccc cgc cag cgc cgc agc Cys Leu Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser 160 165 170	528
gcc ccc ccc agc agc gag gac cac cag aac ctg aat ccc ggc aac gag Ala Pro Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu 175 180 185 190	576
cag gag ctg ctg gag ctg gac aag tgg gcc agc ctg tgg aac tgg ttc Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe 195 200 205	624
gac atc acc ggc cca gga ccc cac gag cgc agc tac atg ttc agc gac Asp Ile Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp 210 215 220	672
ctg gag aac cgc tgc atc aac gag aag gac ctg ctg gcc ctg gac aag Leu Glu Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys 225 230 235	720
tgg cag aac ctg tgg agc tgg ttc gac atc acc aac cct ggc agc ggc Trp Gln Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly 240 245 250	768
atc gtg cag cag cag aac aac ctg ctg cgc gcc atc gag gcc cag cag Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln 255 260 265 270	816
cac ctg ctg cag ctg acc acc gtg tgg ggc atc aag cag ctg cag gcc His Leu Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala 275 280 285	864
cgc atc ctg aat ccc ggc ggt cct gga cca tgg atg gag tgg gac cgc Arg Ile Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg 290 295 300	912
gag atc aac aac tac acc agc ctg atc cac agc ctg atc gag gag agc Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser 305 310 315	960
cag aac cag cag gag aag aac gag cag gag ctg ctg tct aga ccc ggg Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly 320 325 330	1008
ggt acc atg gcc ttc agc ccc gag gtg atc ccc atg ttc agc gcc ctg Gly Thr Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu 335 340 345 350	1056
agc gag ggc gcc acc ccc cag gac ctg ccc atc gtg cag aac atc cag Ser Glu Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln 355 360 365	1104
ggc cag atg gtg cac cag gcc atc agc ccc cgc acc ctg aac gcc ggc Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly 370 375 380	1152

ccc ggc ccc ctg cag gag cag atc ggc tgg atg acc aac aac ccc ccc Pro Gly Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro 385 390 395	1200
atc ccc gtg ggc gag atc tac aag cgc tgg atc atc ctg ggc ctg aac Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn 400 405 410	1248
aag atc gtg cgc atg tac agc ccc acc agc atc ctg gac atc cgc cag Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln 415 420 425 430	1296
ggc ccc aag gag ccc ttc cgc gac tac gtg gac cgc ttc tac aag gag Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu 435 440 445	1344
atc tgc acc gag atg gag aag gag ggc aag atc agc aag atc ggc ccc Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro 450 455 460	1392
ggc ccc ggc ccc ttc cgc aag tac acc gcc ttc acc atc ccc agc atc Gly Pro Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile 465 470 475	1440
aac aac gag agc ccc gcc atc ttc cag agc agc atg acc aag atc ctg Asn Asn Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu 480 485 490	1488
gag ccc tgg gag ttc gtg aac acc ccc ccc ctg gtg aag ctg tgg tac Glu Pro Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr 495 500 505 510	1536
cag aag acc gcc gtg cag atg gcc gtg ttc atc cac aac ttc aag cgc Gln Lys Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg 515 520 525	1584
cag aag cag atc acc aag atc cag aac ttc cgc gtg tac tac cgc ggc Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly 530 535 540	1632
ccc ggc ccc cag ctg ctg ttc atc cac ttc cgc tcg cgc cag cgg cgg Pro Gly Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg 545 550 555	1680
cgg cgg tac agc agc ttg atc agg cgc acg gtg cgg atc agc tcc tcg Arg Arg Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser 560 565 570	1728
tcg cgg ctg tgg cgg cag ccg atg cgg aag tgg atg aac agc agc atc Ser Arg Leu Trp Arg Gln Pro Met Arg Lys Trp Met Asn Ser Ser Ile 575 580 585 590	1776
agc ggc ccc ggc ccc gac atg cgc gac aac tgg cgc agc gag ctg tac Ser Gly Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr 595 600 605	1824
aag tac aag gtg cag cag cac ctg ctg cag ctg acc gtg tgg ggc atc Lys Tyr Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile 610 615 620	1872
aag cag ctg gcc agc ctg tgg aac tgg ttc gac atc acc aac tgg ctg	1920

Lys Gln Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu
 625 630 635
 tgg tac atc aag atc ttc atc atg atc gtg ggc ggc ctg atc ggc ctg 1968
 Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
 640 645 650
 cgc cac atc ccc cgc cgc atc cgc cag ggc ctg gag cgc gcc ctg agg 2016
 Arg His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg
 655 660 665 670
 gca gca tgg acg agg gca ccg ccg acg agc gcg ccc ccc cgc ggc cag 2064
 Ala Ala Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Arg Gly Gln
 675 680 685
 ggc agc atg gac gag ggc acc gcc gac gag cgc gcc ccc ctg atc cgc 2112
 Gly Ser Met Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg
 690 695 700
 acc tga gtttaaacc 2126
 Thr

<210> 8
 <211> 703
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Construct encoding polypeptide.

<400> 8

Met Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln
 1 5 10 15

Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg Ala Pro
 20 25 30

Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala Ala Gln
 35 40 45

Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg Ser Gln
 50 55 60

Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro Pro Cys
 65 70 75 80

Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val Cys Phe
 85 90 95

Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser Asn Lys
 100 105 110

Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu Leu Ala
 115 120 125

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Pro
 130 135 140

Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His Cys Leu
 145 150 155 160

Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser Ala Pro
 165 170 175

Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu Gln Glu
 180 185 190

Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile
 195 200 205

Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp Leu Glu
 210 215 220

Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys Trp Gln
 225 230 235 240

Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly Ile Val
 245 250 255

Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu
 260 265 270

Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile
 275 280 285

Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg Glu Ile
 290 295 300

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
 305 310 315 320

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly Gly Thr
 325 330 335

Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
 340 345 350

Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln Gly Gln
 355 360 365

Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly Pro Gly
 370 375 380

Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
 385 390 395 400

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
 405 410 415

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
 420 425 430

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu Ile Cys
 435 440 445

Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Gly Pro
 450 455 460

Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
 465 470 475 480

Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro
 485 490 495

Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Lys
 500 505 510

Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Gln Lys
 515 520 525

Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly Pro Gly
 530 535 540

Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg Arg Arg
 545 550 555 560

Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser Ser Arg
 565 570 575

Leu Trp Arg Gln Pro Met Arg Lys Trp Met Asn Ser Ser Ile Ser Gly
 580 585 590

Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr

595 600 605

Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln
610 615 620

Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu Trp Tyr
625 630 635 640

Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu Arg His
645 650 655

Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg Ala Ala
660 665 670

Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Arg Gly Gln Gly Ser
675 680 685

Met Asp Glu Gly Thr Ala Asp Glu Arg Ala Pro Leu Ile Arg Thr
690 695 700

<210> 9
<211> 2063
<212> DNA
<213> Artificial Sequence

<220>
<223> Construct encoding polyepitope polypeptide.

<220>
<221> CDS
<222> (7)..(2061)
<223> Sequence encoding MCMVABTh polyepitope polypeptide.

<400> 9
gctagc atg gcc tgc acc aac tgc tac tgc aag aag tgc tgc ttc cac 48
Met Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
1 5 10

tgc cag gtg tgc ttc acc acc ggc ccc ggc ccc cgc cag cgc cgc cgc 96
Cys Gln Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg
15 20 25 30

gcc ccc cag gac agc cag acc cac cag gtg agc gta tac tac gcc gcc 144
Ala Pro Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala
35 40 45

gcc cag tgg gac ttc ggc aac acc atg tgc cag atc aat ccc ggc cgc 192
Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg
50 55 60

agc cag aag gag ggc ctg cac tac acc tgc gta tac ggc ccc ggc ccc 240
Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro
65 70 75

ccc tgc aac aag tgc tac tgc aag aag tgc tgc tac cac tgc cag gtg Pro Cys Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val 80 85 90	288
tgc ttc ctg aac aat ccc ggc aag cag cgc cgc ggc acc ccc cag agc Cys Phe Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser 95 100 105 110	336
aac aag gac cac cag aac ccc ggc cct gga ccc aac gag cag gac ctg Asn Lys Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu 115 120 125	384
ctg gcc ctg gac aag tgg gcc aac ctg tgg aac tgg ttc gac atc agc Leu Ala Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser 130 135 140	432
aat ccc ggc gcc tgc aac acc tgc tac tgc aag aag tgc agc tac cac Asn Pro Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His 145 150 155	480
tgc ctg gtg tgc ttc cag acc ggc ccc ggc ccc cgc cag cgc cgc agc Cys Leu Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser 160 165 170	528
gcc ccc ccc agc agc gag gac cac cag aac ctg aat ccc ggc aac gag Ala Pro Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu 175 180 185 190	576
cag gag ctg ctg gag ctg gac aag tgg gcc agc ctg tgg aac tgg ttc Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe 195 200 205	624
gac atc acc ggc cca gga ccc cac gag cgc agc tac atg ttc agc gac Asp Ile Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp 210 215 220	672
ctg gag aac cgc tgc atc aac gag aag gac ctg ctg gcc ctg gac aag Leu Glu Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys 225 230 235	720
tgg cag aac ctg tgg agc tgg ttc gac atc acc aac cct ggc agc ggc Trp Gln Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly 240 245 250	768
atc gtg cag cag cag aac aac ctg ctg cgc gcc atc gag gcc cag cag Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln 255 260 265 270	816
cac ctg ctg cag ctg acc acc gtg tgg ggc atc aag cag ctg cag gcc His Leu Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala 275 280 285	864
cgc atc ctg aat ccc ggc ggt cct gga cca tgg atg gag tgg gac cgc Arg Ile Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg 290 295 300	912
gag atc aac aac tac acc agc ctg atc cac agc ctg atc gag gag agc Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser 305 310 315	960

cag aac cag cag gag aag aac gag cag gag ctg ctg tct aga ccc ggg Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly 320 325 330	1008
ggt acc atg gcc ttc agc ccc gag gtg atc ccc atg ttc agc gcc ctg Gly Thr Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu 335 340 345 350	1056
agc gag ggc gcc acc ccc cag gac ctg ccc atc gtg cag aac atc cag Ser Glu Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln 355 360 365	1104
ggc cag atg gtg cac cag gcc atc agc ccc cgc acc ctg aac gcc ggc Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly 370 375 380	1152
ccc ggc ccc ctg cag gag cag atc ggc tgg atg acc aac aac ccc ccc Pro Gly Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro 385 390 395	1200
atc ccc gtg ggc gag atc tac aag cgc tgg atc atc ctg ggc ctg aac Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn 400 405 410	1248
aag atc gtg cgc atg tac agc ccc acc agc atc ctg gac atc cgc cag Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln 415 420 425 430	1296
ggc ccc aag gag ccc ttc cgc gac tac gtg gac cgc ttc tac aag gag Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu 435 440 445	1344
atc tgc acc gag atg gag aag gag ggc aag atc agc aag atc ggc ccc Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro 450 455 460	1392
ggc ccc ggc ccc ttc cgc aag tac acc gcc ttc acc atc ccc agc atc Gly Pro Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile 465 470 475	1440
aac aac gag agc ccc gcc atc ttc cag agc agc atg acc aag atc ctg Asn Asn Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu 480 485 490	1488
gag ccc tgg gag ttc gtg aac acc ccc ccc ctg gtg aag ctg tgg tac Glu Pro Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr 495 500 505 510	1536
cag aag acc gcc gtg cag atg gcc gtg ttc atc cac aac ttc aag cgc Gln Lys Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg 515 520 525	1584
cag aag cag atc acc aag atc cag aac ttc cgc gtg tac tac cgc ggc Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly 530 535 540	1632
ccc ggc ccc cag ctg ctg ttc atc cac ttc cgc tcg cgc cag cgg cgg Pro Gly Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg 545 550 555	1680
cgg cgg tac agc agc ttg atc agg cgc acg gtg cgg atc agc tcc tcg	1728

Arg Arg Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser
 560 565 570
 tcg cgg ctg tgg cgg cag ccg atg cgg aag tgg atg aac agc agc atc 1776
 Ser Arg Leu Trp Arg Gln Pro Met Arg Lys Trp Met Asn Ser Ser Ile
 575 580 585 590
 agc ggc ccc ggc ccc gac atg cgc gac aac tgg cgc agc gag ctg tac 1824
 Ser Gly Pro Gly Pro Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
 595 600 605
 aag tac aag gtg cag cag cac ctg ctg cag ctg acc gtg tgg ggc atc 1872
 Lys Tyr Lys Val Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile
 610 615 620
 aag cag ctg gcc agc ctg tgg aac tgg ttc gac atc acc aac tgg ctg 1920
 Lys Gln Leu Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Asn Trp Leu
 625 630 635
 tgg tac atc aag atc ttc atc atg atc gtg ggc ggc ctg atc ggc ctg 1968
 Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly Leu Ile Gly Leu
 640 645 650
 cgc cac atc ccc cgc cgc atc cgc cag ggc ctg gag cgc gcc ctg agg 2016
 Arg His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Arg
 655 660 665 670
 gca gca tgg acg agg gca ccg ccg acg agc gcg ccc ccc gtt taa ac 2063
 Ala Ala Trp Thr Arg Ala Pro Pro Thr Ser Ala Pro Pro Val
 675 680

<210> 10

<211> 684

<212> PRT

<213> Artificial Sequence

<220>

<223> Construct encoding polypeptide polypeptide.

<400> 10

Met Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln
 1 5 10 15

Val Cys Phe Thr Thr Gly Pro Gly Pro Arg Gln Arg Arg Arg Ala Pro
 20 25 30

Gln Asp Ser Gln Thr His Gln Val Ser Val Tyr Tyr Ala Ala Ala Gln
 35 40 45

Trp Asp Phe Gly Asn Thr Met Cys Gln Ile Asn Pro Gly Arg Ser Gln
 50 55 60

Lys Glu Gly Leu His Tyr Thr Cys Val Tyr Gly Pro Gly Pro Pro Cys
 65 70 75 80

Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val Cys Phe
 85 90 95

Leu Asn Asn Pro Gly Lys Gln Arg Arg Gly Thr Pro Gln Ser Asn Lys
 100 105 110

Asp His Gln Asn Pro Gly Pro Gly Pro Asn Glu Gln Asp Leu Leu Ala
 115 120 125

Leu Asp Lys Trp Ala Asn Leu Trp Asn Trp Phe Asp Ile Ser Asn Pro
 130 135 140

Gly Ala Cys Asn Thr Cys Tyr Cys Lys Lys Cys Ser Tyr His Cys Leu
 145 150 155 160

Val Cys Phe Gln Thr Gly Pro Gly Pro Arg Gln Arg Arg Ser Ala Pro
 165 170 175

Pro Ser Ser Glu Asp His Gln Asn Leu Asn Pro Gly Asn Glu Gln Glu
 180 185 190

Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile
 195 200 205

Thr Gly Pro Gly Pro His Glu Arg Ser Tyr Met Phe Ser Asp Leu Glu
 210 215 220

Asn Arg Cys Ile Asn Glu Lys Asp Leu Leu Ala Leu Asp Lys Trp Gln
 225 230 235 240

Asn Leu Trp Ser Trp Phe Asp Ile Thr Asn Pro Gly Ser Gly Ile Val
 245 250 255

Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu
 260 265 270

Leu Gln Leu Thr Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile
 275 280 285

Leu Asn Pro Gly Gly Pro Gly Pro Trp Met Glu Trp Asp Arg Glu Ile
 290 295 300

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
 305 310 315 320

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Ser Arg Pro Gly Gly Thr
 325 330 335

Met Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
 340 345 350

Gly Ala Thr Pro Gln Asp Leu Pro Ile Val Gln Asn Ile Gln Gly Gln
 355 360 365

Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Gly Pro Gly
 370 375 380

Pro Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
 385 390 395 400

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
 405 410 415

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
 420 425 430

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Glu Ile Cys
 435 440 445

Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Gly Pro
 450 455 460

Gly Pro Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
 465 470 475 480

Glu Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro
 485 490 495

Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Lys
 500 505 510

Thr Ala Val Gln Met Ala Val Phe Ile His Asn Phe Lys Arg Gln Lys
 515 520 525

Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Gly Pro Gly
 530 535 540

Pro Gln Leu Leu Phe Ile His Phe Arg Ser Arg Gln Arg Arg Arg Arg
 545 550 555 560

Tyr Ser Ser Leu Ile Arg Arg Thr Val Arg Ile Ser Ser Ser Ser Arg

				565					570							575
Leu	Trp	Arg	Gln	Pro	Met	Arg	Lys	Trp	Met	Asn	Ser	Ser	Ile	Ser	Gly	
			580					585					590			
Pro	Gly	Pro	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	
		595					600					605				
Lys	Val	Gln	Gln	His	Leu	Leu	Gln	Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	
	610					615					620					
Leu	Ala	Ser	Leu	Trp	Asn	Trp	Phe	Asp	Ile	Thr	Asn	Trp	Leu	Trp	Tyr	
625					630					635					640	
Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Ile	Gly	Leu	Arg	His	
				645					650					655		
Ile	Pro	Arg	Arg	Ile	Arg	Gln	Gly	Leu	Glu	Arg	Ala	Leu	Arg	Ala	Ala	
			660					665					670			
Trp	Thr	Arg	Ala	Pro	Pro	Thr	Ser	Ala	Pro	Pro	Val					
		675						680								

```
<210> 11
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 11
```

Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys
1 5 10

```
<210> 12
<211> 13
<212> PRT
<213> Artificial Sequence,

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 12
```

Ala Val Arg His Phe Pro Arg Ile Trp Leu His Ser Leu
1 5 10

<210>	13
<211>	13

<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 13

Ala Val Arg His Phe Pro Arg Pro Trp Leu His Gly Leu
1 5 10

<210> 14
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 14

Glu Arg Tyr Leu Lys Asp Gln Gln Leu
1 5

<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 15

Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Asp Gln Leu
1 5 10 15

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 16

Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile
1 5 10 15

<210> 17
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 17

Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
1 5 10

<210> 18

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 18

Ala Ile Phe Gln Ser Ser Met Thr Lys
1 5

<210> 19

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 19

Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
1 5 10 15

<210> 20

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 20

Arg Ile Arg Thr Thr Trp Lys Ser Leu Val Lys
1 5 10

<210> 21

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 21

Ala Val Arg His Phe Pro Arg Ile Trp Leu His Ser Leu
1 5 10

<210> 22
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 22

Ala Val Arg His Phe Pro Arg Pro Trp Leu His Gly Leu
1 5 10

<210> 23
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 23

Val Ser Asp Gly Gly Pro Asn Leu Tyr
1 5

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 24

Cys Thr Glu Leu Lys Leu Ser Asp Tyr
1 5

<210> 25
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 25

Gly Leu Cys Thr Leu Val Ala Met Leu
1 5

<210> 26
<211> 9
<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 26

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 27

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 27

Asn Leu Val Pro Met Val Ala Thr Val
1 5

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 28

Ile Leu Arg Gly Ser Val Ala His Lys
1 5

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 29

Arg Val Arg Ala Tyr Thr Tyr Ser Lys
1 5

<210> 30

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 30

Arg Leu Arg Ala Glu Ala Gln Val Lys
1 5

<210> 31

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 31

Ile Val Thr Asp Phe Ser Val Ile Lys
1 5

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 32

Ala Thr Ile Gly Thr Ala Met Tyr Lys
1 5

<210> 33

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 33

Asp Tyr Cys Asn Val Leu Asn Lys Glu Phe
1 5 10

<210> 34

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 34

Lys Thr Gly Gly Pro Ile Tyr Lys Arg
1 5

<210> 35
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 35

Arg Pro Pro Ile Phe Ile Arg Arg Leu
1 5

<210> 36
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 36

Thr Pro Arg Val Thr Gly Gly Gly Ala Met
1 5 10

<210> 37
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 37

Gln Ala Lys Trp Arg Leu Gln Thr Leu
1 5

<210> 38
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 38

Phe Leu Arg Gly Arg Ala Tyr Gly Leu
1 5

<210> 39
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 39

Arg Ala Lys Phe Lys Gln Leu Leu
1 5

<210> 40

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 40

Glu Leu Arg Ser-Arg Tyr Trp Ala Ile
1 5

<210> 41

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 41

Ser Arg Tyr Trp Ala Ile Arg Thr Arg
1 5

<210> 42

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 42

Arg Arg Ile Tyr Asp Leu Ile Glu Leu
1 5

<210> 43

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Control peptide.

<400> 43

Tyr Pro Leu His Glu Gln His Gly Met
1 5

<210> 44
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 44

Glu Glu Asn Leu Leu Asp Phe Val Arg Phe
1 5 10

<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Control peptide.

<400> 45

Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala
1 5 10 15

<210> 46
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 46

Pro Cys Asn Lys Cys Tyr Cys Lys Lys Cys Cys Tyr His Cys Gln Val
1 5 10 15

Cys Phe Ile Thr
20

<210> 47
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 47

Ala Cys Ser Lys Cys Tyr Cys Lys Lys Cys Cys Trp His Cys Gln Leu
1 5 10 15

Cys Phe Leu Lys
20

<210> 48
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 48

Pro Cys Thr Lys Cys Tyr Cys Lys Arg Cys Cys Phe His Cys Gln Trp
1 5 10 15

Cys Phe Ile Thr
20

<210> 49
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 49

Ala Cys Ser Lys Cys Tyr Cys His Ile Cys Cys Trp His Cys Gln Leu
1 5 10 15

Cys Phe Leu Asn
20

<210> 50
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV-1 antigenic fragment/epitope.

<400> 50

Arg Gln Arg Arg Arg Pro Pro Gln Gly Gly Gln Ala His Gln Asp Pro
1 5 10 15

<210> 51
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 51

Lys	His	Arg	Arg	Gly	Thr	Pro	Gln	Ser	Ser	Lys	Asp	His	Gln	Asn	Pro
1				5					10					15	

<210> 52

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 52

Arg	Arg	Arg	Arg	Gly	Thr	Pro	Gln	Ser	Arg	Gln	Asp	His	Gln	Asn	Pro
1				5					10					15	

<210> 53

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 53

Arg	Gln	Arg	His	Arg	Thr	Pro	Gln	Ser	Ser	Gln	Ile	His	Gln	Asp	Pro
1				5					10					15	

<210> 54

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 54

Asn	Glu	Lys	Glu	Leu	Leu	Glu	Leu	Asp	Lys	Trp	Ala	Ser	Leu	Trp	Asn
1				5					10					15	

Trp	Phe	Ser	Ile	Thr
				20

<210> 55

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 55

Asn Glu Gln Glu Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Asn
 1 5 10 15

Trp Phe Asp Ile Ser
 20

<210> 56

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 56

Asn Glu Gln Asp Leu Leu Ala Leu Asp Lys Trp Ala Ser Leu Trp Thr
 1 5 10 15

Trp Phe Ser Ile Thr
 20

<210> 57

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 57

Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala
 1 5 10 15

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
 20 25 30

Ala Arg Ile Leu
 35

<210> 58

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 58

Tyr Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu
1 5 10 15

<210> 59

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 59

Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe
1 5 10 15

Gln Thr Leu Lys
20

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 60

Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro
1 5 10 15

<210> 61

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 61

Gln Leu Leu Phe Ile His Phe Arg Ile Gly Cys Arg His Ser Arg
1 5 10 15

<210> 62

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 62

Asp Glu Glu Leu Ile Arg Thr Val Arg Leu Ile Lys Leu Leu Tyr
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 63

Arg Arg Arg Arg Trp Arg Glu Arg Gln Arg Gln Ile His Ser Ile Ser
1 5 10 15

<210> 64

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 antigenic fragment/epitope.

<400> 64

His Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ala Leu Leu
1 5 10 15